

ABSTRACT

A system and related methods are described for determining a three-dimensional protein structure. In certain embodiments, the methods include predicting the secondary structure for protein of known amino acid sequence, superimposing the secondary structure on a topomer model, and refining the topomer model. In other embodiments, a machine readable medium may provide instructions, which when executed by a machine cause said machine to perform a method including predicting a secondary structure for a protein of known amino acid sequence, superimposing the secondary structure on a topomer model, and refining the topomer model.

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